

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANADOS, EDWARD N.
HAYDEN, MARK
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
- (ii) TITLE OF THE INVENTION: REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE GASTROINTESTINAL
TRACT
- (iii) NUMBER OF SEQUENCES: 49
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Abbott Laboratories
 - (B) STREET: 100 Abbott Park Road
 - (C) CITY: Abbott Park
 - (D) STATE: IL
 - (E) COUNTRY: USA
 - (F) ZIP: 60064-3500
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/828,855
 - (B) FILING DATE: 31-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Becker, Cheryl L.
 - (B) REGISTRATION NUMBER: 35,441
 - (C) REFERENCE/DOCKET NUMBER: 6065.US.P1
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 847/935-1729
 - (B) TELEFAX: 847/938-2623
 - (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCTGCCTGCA CCCGCTCACC CTGAGCGCCT TGGGGTGGTG GGAGGCGCTG GAATCCCCAC
TGTGCAG

60
67

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGAGGCTGCA GACTGTGGAG CCGGGAGCCG GCAG

34

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1841 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAGTAAGCCC	AGAGGTCTCC	ACCCACGCGG	AGGAAGGCTG	AGGCCAAGAC	CCCGGAAGAG	60
ATGGACCGCG	TGACCAGATA	CCCCATCCTG	GGCATCCCTC	AGGCACACCG	TGGCACCGGC	120
CTGGTGCTGG	ATGGAGACAC	CAGCTACACA	TACCATCTGG	TGTGCATGGG	CCCCGAGGCC	180
AGCGGCTGGG	GCCAGGATGA	GCCGACAGACA	TGGCCCACTG	ACCACAGGGC	CCAGCAGGGC	240
GTGCAGAGGC	AGGGGGTGTC	CTACAGCGTG	CATGCCTACA	CTGGCCAGCC	GTCCCCACGG	300
GGGCTCCACT	CGGAGAACAG	GGAGGATGAG	GGTTGGCAGG	TTTACCGCCT	GGGCGCCAGG	360
GATGCCCCAC	AGGGACGTCC	AACATGGGCA	CTCCGCCAG	AGGACGGGGA	GGACAAGGAG	420
ATGAAGACCT	ACCGCTGGA	TGCTGGGGAC	GCTGACCCCA	GGAGGCTGTG	TGACCTGGAG	480
CGGGAGCGCT	GGGCCGTCAT	CCAGGGCCAG	GCAGTCAGGA	AGAGCAGCAC	CGTGGCCACG	540
CTCCAGGGCA	CTCCTGACCA	CGGAGACCCC	AGGACCCCCG	GCCCACCTCG	GTCCACGCCC	600
CTGGAGGAGA	ACGTGGTTGA	CAGGGAGCAG	ATTGACTTCC	TGGCAGCGAG	ACAGCAGTTC	660
CTGAGTCTGG	AGCAGGCGAA	CAAGGGGGCC	CCTCATAGCT	CCCCGGCCAG	GGGGACCCCT	720
GCAGGCACAA	CCCCAGGGGC	CAGCCAGGCC	CCCAAGGCCT	TCAACAAGCC	CCACCTGGCC	780
AACGGGCACG	TGGTTCCCAT	CAAGCCCCAG	GTGAAGGGGG	TGGTCAGGGA	AGAGAACAAG	840
GTGCGTGCTG	TGCCCCACCTG	GGCCAGTGTC	CAAGTTGTGG	ATGACCCTGG	CTCCTTGGCC	900
TCAGTGGAGT	CCCCGGGGAC	CCCCAAGGAG	ACGCCCATCG	AGCGGGAGAT	CCGTCTGGCT	960
CAGGAGCGTG	AGGCAGACCT	GCGAGAGCAG	AGGGGGCTTC	GGCAGGCAAC	CGACCACCAG	1020
GAGCTGGTGG	AAATCCCCAC	CAGGCCGCTG	CTGACCAAGC	TGAGCCTGAT	CACAGCCCCA	1080
CGGCGGGAGA	GAGGGCGCCC	GTCCCTCTAC	GTGCAGCGGG	ACATAGTACA	GGAGACACAG	1140
CGTGAGGAAG	ACCACCGGCG	GGAGGGCCTG	CACGTGGGCC	GGGCGTCCAC	ACCCGACTGG	1200
GTCTCGGAGG	GTCCCCAGCC	CGGACTCCGG	AGAGCCCTCA	GCTCAGATTG	CATCCTCAGC	1260
CCGGCCCCAG	ATGCCCGTGC	GGCCGACCCA	GCTCCAGAAG	TGAGGAAGGT	GAACCGCATC	1320
CCACCTGATG	CCTACCAGCC	GTACCTGAGC	CCCGGGACCC	CCCAGCTAGA	ATTCTCAGCC	1380
TTCGGAGCAT	TCGGCAAGCC	CAGCAGTCTC	TCCACAGCGG	AGGCCAAGGC	TGCGACTTCA	1440
CCAAAGGCCA	CGATGTCCCC	GAGGCATCTC	TCAGAATCCT	CTGGAAAACC	CCTGAGCACA	1500
AAGCAAGAGG	CATCGAAGCC	CCCTCGGGGA	TGCCCGCAAG	CCAACAGGGG	TGTCGTGCGG	1560
TGGGAGTACT	TCCGCCTGCG	TCCTCTGCGG	TTCAGGGCCC	CAGACGAGCC	CCAGCAGGCC	1620
CAAGTCCCCC	ATGTCTGGGG	CTGGGAGGTG	GCTGGGGCCC	CTGCACTGAG	GCTGCAGAAG	1680

TCCCAGTCAT	CTGATCTGCT	GGAAAGGGAG	AGGGAGAGTG	TCCTGCGCCG	GGAGCAAGAG	1740
GTGGCAGAGG	AGCGGAGAAA	TGCTCTCTTC	CCAGAGGTCT	TCTCCCCAAC	GCCAGATGAG	1800
AACTCTGACC	AGAACTCCAG	GAGCTCCTCC	CAGGCATCCG	G		1841

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGCATCACGG	GCAGTTACTC	GGTGTCTGAG	TCTCCCTTCT	TCAGCCCCAT	CCACCTACAC	60
TCAAACGTGG	CGTGGACAGT	GGAAGATCCA	GTGGACAGTG	CTCCTCCCCG	GCAGAGAAAG	120
AAGGAGCAAT	GG					132

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTACGCTGGC	ATCAACCCCT	CGGACGGTAT	CAACTCAGAG	GT		42
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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 820 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGGTCCTGGA	AGCCATACGG	GTGACCCGTC	ACAAGAACGC	CATGGCAGAG	CGCTGGGAAT	60
CCCGCATCTA	CGCCAGTGAG	GAGGATGACT	GAGCCTCGGG	ATGGGGCGCC	CACCCCCTGC	120
CCTGCCCTGA	CCCTCGTGGG	AACTGCCAAG	ACCATCGCCA	AGCCCCCACC	CTAGGAAATG	180
GGTCCTAGGT	CCAGGATCCA	AGAACCACAG	CTCATCTGCC	AACAATCCCA	CCATGGGCAC	240
ATTTGGGACT	GTTGGGTTTT	TCGTTTCCGT	TTCTATCTTC	CTTTAGAAAT	GTTTCTGCCT	300
TTGGGGTCTA	AAGCTTTTGG	GGATGAAATG	GGACCCCTGC	TGATTCTTTC	TGCTTCTAAG	360
ACTTTGCCAA	ATGCCCTGGG	TCTAAGAAAG	AAAGAGACCC	GCTCCTCCAC	TTTCAGGTGT	420
AATTTGCTTC	CGCTAGTCTG	AGGGCAGAGG	GACCGGTCAA	AGAGGGTGGC	ACAGATCGCA	480
GCACCTTGAG	GGGCTGCGGG	TCTGAGGGAG	GAGACACTCA	GCTCCTCCCT	CTGAGAAGTC	540
CCAAGCTGAG	AGGGGAGACC	TGCCCCTTTC	CAACCCTGGG	AAACCATCCA	GTCTGAGGGA	600
GGAGGCCAAA	CTCCCAGTGC	TGGGGGTCCC	TGTGCAGCCC	TCAAACCCTT	CACCTTGGTG	660
CACCCAGCCA	CACCTGGTGG	ACACAAAGCT	CTCACATCGA	TAGGATCCCA	TGAGGATGGT	720
CCCCTTCACC	TGGGAGAAAA	GTGACCCAGT	TTAGGAGCTG	GAGGGGGGTC	TTTGTCCCCC	780
ACCCCCAAAC	TGCCCTGAAA	TAAACCTGGA	GTGAGCTGCC			820

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 25
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"
- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 86
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"
- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 87
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"
- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 131
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"
- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 155
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"
- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 254
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"
- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 259
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCTGCCTGCA	CCCCTCACC	CTGANCCT	TGGGGTGGTG	GGAGGCGCTG	GAATCCCCAC	60
TGTGCAGTAA	GCCCAGATGT	CTCCANNCCA	ACGGTAGGAA	GGCTGATGCC	AAGACCCCGG	120
AAGAGATGGA	NCGCGTGACC	AGATACCCAT	CCTGNGCATC	CCTCAGGCAC	ACCGTGGCAC	180
CGGCCTGGTG	CTGGATGGAG	ACACCAGCTA	CACATACCAT	CTGGTGTGCA	TTGGCCCCGA	240
AGCCAGCGGC	TGGNGCCANG	ATGAGCCGCA	ACATGGCCAC	T		281

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 45
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"
- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism

- (B) LOCATION: 195
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 207
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 212
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 243
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:
 - (A) NAME/KEY: base_polymorphism
 - (B) LOCATION: 286
 - (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCTGCCTGCA	CCCGCTTCAC	CCTGAGCGCC	TTGGGGTGGT	GGGANGCGCT	GGAATCCCCA	60
CTGTGCAGTA	AGCCCAGAGG	TCTCCACCCC	ACGGGATGAA	GGCTGAGGCC	AAGACCCCGG	120
AAGAGATGGA	CCGCGTGACC	AGATACCCCA	TCCTGGGCAT	CCCTCAGGCA	CACCGTGGGC	180
ACCGGCCTGG	TGCTNGATGG	AGACACNAGT	TNCACATACC	ATCTGGTGTG	CATGGGCCCC	240
GANGCAGCGG	TGGGCGAGGA	TGAGCCGCG	ACATGGCCAC	TGACCNAAGG	CCAT	294

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGAGGCTGCA	GACTGTGGAG	CCGGGAGCCG	GCAGTAAGCC	CAGAGGTCTC	CACCCACGG	60
GAGGAAGGCT	GAGGCCAAGA	CCCCGGAAGA	GATGGACCGC	GTGACCAGAT	ACCCCATCCT	120
GGGCATCCCT	CAGGCACACC	GTGGCACC	GG T			151

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGCAGACTGT	GGAGCCGGGA	GCCGGCAGTA	AGCCCAGAGG	TCTCCACCCC	ACGGGAGGAA	60
GGCTGAGGCC	AAGACCCCGG	AAGAGATGGA	CCGCGTGACC	AGATACCCCA	TCCTGGGC	118

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCAGACTGT	GGAGCCGGGA	GCCGGCAGTA	AGCCCAGAGG	TCTCCACCCC	ACGGGAGGAA	60
GGCTGAGGCC	AAGACCCCGG	AAGAGATGGA	CCGCGTGACC	AGATACCCCA	TCCTGGGCAT	120
CCCTCAGGCA	CACCGTGGCA	CCGGCCTGGT	GCTGGATGGA	GACACCAGCT	ACACATACCA	180
TCTGGTGTGC	ATGGGCCCCG	AGGCCAGCGG	TGGGGCCAGG	ATG		223

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CCCCGGAAGA	GATGGACCGC	GTGACCAGAT	ACCCCATCCT	GGGCATCCCT	CAGGCACACC	60
GTGGCACCGG	CCTGGTGCTG	GATGGAGACA	CCAGCTACAC	ATACCATCTG	GTGTGCATGG	120
GCCCCGAGGC	CAGCGGCTGG	GGCCAGGATG	AGCCGAGAC	ATGGCCCACT	GACCACAGGG	180
CCCAGCAGGG	CGTGCAGAGG	CAGGGGGTGT	CCTACAGCGT	GCATGCCTAC	ACTGGCCAGC	240
CGTCCCCACG	GGGGCTC					257

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAGGGCCAGC	GGCTGGGGCC	AGGATGAGCC	GCAGACATGG	CCCACTGACC	ACAGGGCCCA	60
GCAGGGCGTG	CAGAGGCAGG	GGGTGTCTTA	CAGCGTGCAT	GCCTACACTG	GCCAGCCGTC	120
CCCACGGGGG	CTCCACTCGG	AGAACAGGGA	GGATGAGGGT	TGGCAGGTTT	ACCGCCTGGG	180
CGCCAGGGAT	GCCCACCAGG	GACGTCCAAC	ATGGGCACTC	CGCCCAGAGG	ACGGGGAGGA	240
CAAGGAGATG	AAGACCTACC	GCCTGGATGC	TGGGGACGCT	GACCCCAGGA	GGCTGTGTGA	300
CTGGAG						306

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GCTGTCTCGC	TGCCAGGAAG	TCAATCTGCT	CCCTGTCAAC	CACGTTCTCC	TCCAGGGGCG	60
TGGACCGAGG	TGGGCCGGGG	GTCCTGGGGT	CTCCGTGGTC	AGGAGTGCCC	TGGAGCGTGG	120
CCACGGTGCT	GCTCTTCCTG	ACTGCCTGGC	CCTGGATGAC	GGCCCAGCGC	TCCCGCTCCA	180
GGTCACACAG	CCTCCTGGGG	TCAGCGTCCC	CAGCATCCAG	GCGGTAGGTC	TTCATCTCCT	240

TGTCCTCCCC GTCCTCTGGG C

261

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 41
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGAGCAGGCG	AACAAGGGGG	CCCCTCATAG	CTCCCCGGCC	NGGGGGACCC	CTGCAGGCAC	60
AACCCAGGG	GCCAGCCAGG	CCCCAAGGC	CTTCAACAAG	CCCCACCTGG	CCAACGGGCA	120
CGTGTTCCC	ATCAAGCCCC	AGGTGAAGGG	GGTGGTCAGG	GAAGAGAACA	AGGTGCGTGC	180
TGTGCCACC	TGGGCCAGTG	TCCAAGTTGT	GGATGACCCT	GGCTCCTTGG	CCTCAGTGGA	240
GTCCCCGGG	ACCCCAAGG	AGACGCCCAT	CGAGCGGGAG	ATCCGTCTGG	CTCAG	295

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 260
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TGCAGCGGNG	ACATAGTACA	GGAGACACAG	CGTGAGGAAG	ACCACCGGCG	GGAGGGCCTG	60
CACGTGGGCC	GGGCGTCCAC	ACCCGACTGG	GTCTCGGAGG	GTCCCCAGCC	CGGACTCCGG	120
AGAGCCCTCA	GCTCAGATTC	CATCCTCAGC	CCGGCCCCAG	ATGCCCCGTGC	GGCCGACCCA	180
GCTCCAGAAG	TGAGGAAGGT	GAACCGCATC	CCACCTGATG	CCTACCAGCC	GTACCTGAGC	240
CCCGGGACCC	CCCAGCTAGN	ATTCTCAGCT	TCGGAGCATT	CGGCAAGCCC	AG	292

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 89
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

- (ix) FEATURE:
 (A) NAME/KEY: base_polymorphism
 (B) LOCATION: 101
 (D) OTHER INFORMATION: /note= "'N' represents an A or G or
 T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CTGATGCCTA	CCAGCCGTAC	CTGAGCCCCG	GGACCCCCCA	GCTAGAATTC	TCAGCCTTCG	60
GAGCATTCGG	CAAGCCCAGC	AGTCTCTCNA	CAGCGGAGGA	NCAAGGCTGC	GACTTCACCA	120
AAGGCCACGA	TGTCCCCGAG	GCATCTCTCA	GAATCCTCTG	GAAAACCCCT	GAGCACAAAG	180
CAAGAGGCAT	CGAAGCCCC	TCGGGGATGC	CCGCAAGCCA	ACAGGG		226

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCTCCACAG	CGGAGGCCAA	GGCTGCGACT	TCACCAAAGG	CCACGATGTC	CCCGAGGCAT	60
CTCTCAGAAT	CCTCTGGAAA	ACCCCTGAGC	ACAAAGCAAG	AGGCATCGAA	GCCCCCTCGG	120
GGATGCCCGC	AAGCCAACAG	GGGTGTCGTG	CGGTGGGAGT	ACTTCCGCCT	GCGTCCTCTG	180
CGGTCAGGG	CCCCAGACGA	GCCCCA				206

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: base_polymorphism
 (B) LOCATION: 84
 (D) OTHER INFORMATION: /note= "'N' represents an A or G or
 T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGGGGATGCC	CGCAAGCCAA	CAGGGGTGTC	GTGCGGTGGG	AGTACTTCCG	CCTGCGTCCT	60
CTGCGGTTCA	GGGCCCCAGA	CGANCCCCAG	CAGGCCCAAG	TCCCCCATGT	CTGGGGCTGG	120
GAGGTGGCTG	GGGCCCCCTG	ACTGAGGCTG	CAGAAATCCC	AGTCATCTGA	TCTGCTGGAA	180
AGGGAGAGGG	AGAGTGTCTT	GCGCCGGGAG	CAAGAGGTGG	CAGAGGAGCG	GAGAAATGCT	240
CTCTTCCCAG	AGGTCTTC					258

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ix) FEATURE:
 (A) NAME/KEY: base_polymorphism
 (B) LOCATION: 19
 (D) OTHER INFORMATION: /note= "'N' represents an A or G or
 T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGAGGTGGCT	GGGGCCCCNG	CACTGAGGCT	GCAGAAGTCC	CAGTCATCTG	ATCTGCTGGA	60
AAGGGAGAGG	GAGAGTGTCC	TGCGCCGGGA	GCAAGAGGTG	GCAGAGGAGC	GGAGAAATGC	120
TCTCTTCCCA	GAGGTCTTCT	CCCCAACGCC	AGATGAGAAC	TCTGACCAGA	ACTCCAGGAG	180
CTCCTCCAG	GCATCCGGCA	TCACGGGCAG	TTATCGGTGT	CTGAGTCTCC	CTT	233

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCCCTTCTT	CAGCCCCATC	CACCTACACT	CAAACGTGGC	GTGGACAGTG	GAAGATCCAG	60
TGGACAGTGC	TCCTCCCGGG	CAGAGAAAGA	AGGAGCAATG	GTACGCTGGC	ATCAACCCCT	120
CGGACGGTAT	CAACTCAGAG	GTCCTGGAAG	CCATACGGGT	GACCCGTCAC	AAGAACGCCA	180
TGGCAGAGCG	CTGGGAATCC	CGCATCTACG	CCAGTGAGGA	GGATGACTGA	GCCTCGGGAT	240
GGGGCGCCCA	CCCCCTGCCC	TGCCCTGACC	CTCGTG			277

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: base_polymorphism
- (B) LOCATION: 56
- (D) OTHER INFORMATION: /note= "'N' represents an A or G or T or C polymorphism at this position"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTGGGAATCC	CGCATCTACG	CCAGTGAGGA	GGATGACTGA	GCCTCGGGAT	GGGGCNCCCA	60
CCCCCTGCCC	TGCCCTGACC	CTCGTGGGAA	CTGCCAAGAC	CATCGCCAAG	CCCCACCCT	120
AGGAAATGGG	TCCTAGGTCC	AGGATCCAAG	AACCACAGCT	CATCTGCCAA	CAATCCCACC	180
ATGGGCACAT	TTGGGACTGT	TGGGTTTTTC	GTTTCCGTTT	CTATCTTCCT	TTAGAAATGT	240
TTCTGCCTTT	GGGGTCTAAA	GCTTTTGGGG	ATGAAATGGG	ACCC		284

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCTTTTGGGG	ATGAAATGGG	ACCCCTGCTG	ATTCTTTCTG	CTTCTAAGAC	TTTGCCAAAT	60
GCCCTGGGTC	TAAGAAAGAA	AGAGACCCGC	TCCTCCACTT	TCAGGTGTAA	TTTGCTTCCG	120
CTAGTCTGAG	GGCAGAGGGA	CCGGTCAAAG	AGGGTGGCAC	AGATCGCAGC	ACCTTGAGGG	180
GCTGCGGGTC	TGAGGGAGGA	GACACTCAGC	TCCTCCCTCT	GAGAAGTCCC	AAGCTGAGAG	240
GGGAGACCTG	CCCCTTTCCA	ACCCTGGGAA	ACCATCCAGT	CTGAGGGAGG	AGGCCAAACT	300
TCCAGTGCTG	GGGGTCCCTG	TGCA				324

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAAGAAAGA	GACCCGCTCC	TCCACTTTCA	GGTGTAATTT	GCTTCCGCTA	GTCTGAGGGC	60
AGAGGGACCG	GTCAAAGAGG	GTGGCACAGA	TCGCAGCACC	TTGAGGGGCT	GCGGGTCTGA	120
GGGAGGAGAC	ACTCAGCTCC	TCCCTCTGAG	AAGTCCCAAG	CTGAGAGGGG	AGACCTGCCC	180
CTTTCCAACC	CTGGGAAACC	ATCCAGTCTG	AGGGAGGAGG	CCAAACTCCC	AGTGCTGGGG	240
GTCCCTGTGC	AGCCCTCAAA	CCCTTC				266

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGTCCCTGTG	CAGCCCTCAA	ACCCTTCACC	TTGGTGCACC	CAGCCACACC	TGGTGGACAC	60
AAAGCTCTCA	CATCGATAGG	ATCCCATGAG	GATGGTCCCC	TTCACCTGGG	AGAAAAGTGA	120
CCCAGTTTAG	GAGCTGGAGG	GGGGTCTTTG	TCCCCCACC	CCAAACTGCC	CTGAAATAAA	180
CCTGGAGTGA	GCTGCC					196

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GTCGACCCAC	GCGTCCGCCC	ACGCGTCCGC	GGACGCGTGG	GCTGATGCCT	ACCAGCCGTA	60
CCTGAGCCCC	GGGACCCCCC	AGCTAGAATT	CTCAGCCTTC	GGAGCATTCT	GCAAGCCCAG	120
CAGTCTCTCC	ACAGCGGAGG	CCAAGGCTGC	GACTTCACCA	AAGGCCACGA	TGTCCCCGAG	180
GCATCTCTCA	GAATCCTCTG	GAAAACCCCT	GAGCACAAAG	CAAGAGGCAT	GGAAGCCCCC	240
TCGGGGATGC	CCGCAAGCCA	ACAGGGGTGT	CGTGCGGTGG	GAGTACTTCC	GCCTGCGTCC	300
TCTGCGGTTT	AGGGCCCCAG	ACGAGCCCCA	GCAGGCCCAA	GTCCCCCATG	TCTGGGGCTG	360
GGAGGTGGCT	GGGGCCCCCT	CACTGAGGCT	GCAGAAGTCC	CAGTCATCTG	ATCTGCTGGA	420
AAGGGAGAGG	GAGAGTGTCC	TGCGCCGGGA	GCAAGAGGTG	GCAGAGGAGC	GGAGAAATGC	480
TCTCTTCCCA	GAGGTCTTCT	CCCCAACGCC	AGATGAGAAC	TCTGACCAGA	ACTCCAGGAG	540
CTCCTCCCAG	GCATCCGGCA	TCACGGGCAG	TTACTCGGTG	TCTGAGTCTC	CCTTCTTCAG	600
CCCCATCCAC	CTACACTCAA	ACGTGGCGTG	GACAGTGGAA	GATCCAGTGG	ACAGTGCTCC	660
TCCCGGGCAG	AGAAAGAAGG	AGCAATGGTA	CGCTGGCATC	AACCCCTCGG	ACGGTATCAA	720
CTCAGAGGTC	CTGGAAGCCA	TACGGGTGAC	CCGTCACAAG	AACGCCATGG	CAGAGCGCTG	780
GGAATCCCGC	ATCTACGCCA	GTGAGGAGGA	TGACTGAGCC	TCGGGATGGG	GCGCCCACCC	840
CCTGCCCTGC	CCTGACCCTC	GTGGGAACCTG	CCAAGACCAT	CGCCAAGCCC	CCACCTAGG	900
AAATGGGTCC	TAGGTCCAGG	ATCCAAGAAC	CACAGCTCAT	CTGCCAACAA	TCCCACCATG	960
GGCACATTTG	GGACTGTTGG	GTTTTTCGTT	TCCGTTTCTA	TCTTCCTTTA	GAAATGTTTC	1020
TGCCTTTGGG	GTCTAAAGCT	TTTGGGGATG	AAATGGGACC	CCTGCTGATT	CTTTCTGCTT	1080
CTAAGACTTT	GCCAAATGCC	CTGGGTCTAA	GAAAGAAAGA	GACCCGCTCC	TCCACTTTCA	1140
GGTGTAATTT	GCTTCCGCTA	GTCTGAGGGC	AGAGGGACCG	GTCAAAGAGG	GTGGCACAGA	1200
TCGCAGCACC	TTGAGGGGCT	GCGGGTCTGA	GGGAGGAGAC	ACTCAGCTCC	TCCCTCTGAG	1260
AAGTCCCAAG	CTGAGAGGGG	AGACCTGCCC	CTTTCCAACC	CTGGGAAACC	ATCCAGTCTG	1320
AGGGAGGAGG	CCAAACTCCC	AGTGCTGGGG	GTCCCTGTGC	AGCCCTCAAA	CCCTTCACCT	1380
TGGTGCACCC	AGCCACACCT	GGTGGACACA	AAGCTCTCAC	ATCGATAGGA	TCCCATGAGG	1440
ATGGTCCCCT	TCACCTGGGA	GAAAAGTGAC	CCAGTTTAGG	AGCTGGAGGG	GGGTCTTTGT	1500

CCCCACCCC CAAACTGCCC TGAAATAAAC CTGGAGTGAG CTGCCCA

1547

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCTGCCTGCA	CCCCTCACC	CTGAGCGCCT	TGGGGTGGTT	GCAGACTGTG	GAGCCGGGAG	60
CCGGCAGTAA	GCCCAGAGGT	CTCCACCCCA	CGGGAGGAAG	GCTGAGGCCA	AGACCCCGGA	120
AGAGATGGAC	CGCGTGACCA	GATACCCCAT	CCTGGGCATC	CCTCAGGCAC	ACCGTGGCAC	180
CGGCCTGGTG	CTGGATGGAG	ACACCAGCTA	CACATACCAT	CTGGTGTGCA	TGGGCCCCGA	240
GGCCAGCGGC	TGGGGCCAGG	ATGAGCCGCA	GACATGGCCC	ACTGACCACA	GGGCCCAGCA	300
GGGCGTGCAG	AGGCAGGGGG	TGTCCTACAG	CGTGCATGCC	TACACTGGCC	AGCCGTCCCC	360
ACGGGGGCTC	CACTCGGAGA	ACAGGGAGGA	TGAGGGTTGG	CAGGTTTACC	GCCTGGGCGC	420
CAGGGATGCC	CACCAGGGAC	GTCCAACATG	GGCACTCCGC	CCAGAGGACG	GGGAGGACAA	480
GGAGATGAAG	ACCTACCGCC	TGGATGCTGG	GGACGCTGAC	CCCAGGAGGC	TGTGTGACCT	540
GGAGCGGGAG	CGCTGGGCCG	TCATCCAGGG	CCAGGCAGTC	AGGAAGAGCA	GCACCGTGGC	600
CACGCTCCAG	GGCACTCCTG	ACCACGGAGA	CCCCAGGACC	CCCGGCCAC	CTCGGTCCAC	660
GGCCCTGGAG	GAGAACGTGG	TTGACAGGGA	GCAGATTGAC	TTCCTGGCAG	CGAGACAGCA	720
GTTCTTGAGT	CTGGAGCAGG	CGAACAAGGG	GGCCCCCAT	AGCTCCCCGG	CCAGGGGGAC	780
CCCTGCAGGC	ACAACCCAG	GGGCCAGCCA	GGCCCCAAG	GCCTTCAACA	AGCCCCACCT	840
GGCCAACGGG	CACGTGGTTC	CCATCAAGCC	CCAGGTGAAG	GGGGTGGTCA	GGGAAGAGAA	900
CAAGGTGCGT	GCTGTGCCCA	CCTGGGCCAG	TGTCCAAGTT	GTGGATGACC	CTGGCTCCTT	960
GGCCTCAGTG	GAGTCCCCGG	GGACCCCCAA	GGAGACGCCC	ATCGAGCGGG	AGATCCGTCT	1020
GGCTCAGGAG	CGTGAGGCAG	ACCTGCGAGA	GCAGAGGGGG	CTTCGGCAGG	CAACCGACCA	1080
CCAGGAGCTG	GTGGAAATCC	CCACCAGGCC	GCTGCTGACC	AAGCTGAGCC	TGATCACAGC	1140
CCCACGGCGG	GAGAGAGGGC	GCCCCGTCCCT	CTACGTGCAG	CGGGACATAG	TACAGGAGAC	1200
ACAGCGTGAG	GAAGACCACC	GGCGGGAGGG	CCTGCACGTG	GGCCGGGCGT	CCACACCCGA	1260
CTGGGTCTCG	GAGGGTCCCC	AGCCCGTACT	CCGGAGAGCC	CTCAGCTCAG	ATTCCATCCT	1320
CAGCCCGGCC	CCAGATGCCC	GTGCGGCCGA	CCCAGCTCCA	GAAGTGAGGA	AGGTGAACCG	1380
CATCCACCT	GATGCCTACC	AGCCGTACCT	GAGCCCCGGG	ACCCCCCAGC	TAGAATTCTC	1440
AGCCTTCGGA	GCATTCGGCA	AGCCCAGCAG	TCTCTCCACA	GCGGAGGCCA	AGGTGCGGAC	1500
TTCACCAAAG	GCCACGATGT	CCCCGAGGCA	TCTCTCAGAA	TCCTCTGGAA	AACCCCTGAG	1560
CACAAAGCAA	GAGGCATCGA	AGCCCCCTCG	GGGATGCCCG	CAAGCCAACA	GGGGTGTCTG	1620
GCGGTGGGAG	TACTTCCGCC	TGCGTCTCT	GCGGTTCAGG	GCCCCAGACG	AGCCCCAGCA	1680
GGCCCAAGTC	CCCCATGTCT	GGGGCTGGGA	GGTGGCTGGG	GCCCCCTGCAC	TGAGGCTGCA	1740
GAAGTCCCAG	TCATCTGATC	TGCTGGAAAG	GGAGAGGGAG	AGTGTCTCTG	GCCGGGAGCA	1800
AGAGGTGGCA	GAGGAGCGGA	GAAATGCTCT	CTTCCAGAG	GTCTTCTCCC	CAACGCCAGA	1860
TGAGAACTCT	GACCAGAACT	CCAGGAGCTC	CTCCCAGGCA	TCCGGCATCA	CGGGCAGTTA	1920
CTCGGTGTCT	GAGTCTCCCT	TCTTCAGCCC	CATCCACCTA	CACTCAAACG	TGGCGTGGAC	1980
AGTGGAAAGAT	CCAGTGGACA	GTGCTCCTCC	CGGCAGAGAG	AAGAAGGAGC	AATGGTACGC	2040
TGGCATCAAC	CCCTCGGACG	GTATCAACTC	AGAGGTCCTG	GAAGCCATAC	GGGTGACCCG	2100
TCACAAGAAC	GCCATGGCAG	AGCGCTGGGA	ATCCCCGATC	TACGCCAGTG	AGGAGGATGA	2160
CTGAGCCTCG	GGATGGGGCG	CCCACCCCCT	GCCCTGCCCT	GACCCTCGTG	GGAAGTGCCA	2220
AGACCATCGC	CAAGCCCCCA	CCCTAGGAAA	TGGGTCTTAG	GTCCAGGATC	CAAGAACCAC	2280
AGCTCATCTG	CCAACAATCC	CACCATGGGC	ACATTGGGGA	CTGTTGGGTT	TTTCGTTTCC	2340
GTTTCTATCT	TCCTTTAGAA	ATGTTTCTGC	CTTTGGGGTC	TAAAGCTTTT	GGGGATGAAA	2400
TGGGACCCCT	GCTGATTCTT	TCTGCTTCTA	AGACTTTGCC	AAATGCCCTG	GGTCTAAGAA	2460
AGAAAGAGAC	CCGCTCCTCC	ACTTTCAGGT	GTAATTTGCT	TCCGCTAGTC	TGAGGGCAGA	2520
GGGACCGGTC	AAAGAGGGTG	GCACAGATCG	CAGCACCTTG	AGGGGCTGCG	GGTCTGAGGG	2580
AGGAGACACT	CAGCTCCTCC	CTCTGAGAA	TCCCAAGCTG	AGAGGGGAGA	CCTGCCCCCT	2640
TCCAACCCTG	GGAAACCATC	CAGCTGAGG	GAGGAGGCCA	AACTCCAGT	CTGGGGGCTC	2700
CCTGTGCAGC	CCTCAAACCC	TTCACCTTGG	TGCACCCAGC	CACACCTGGT	GGACACAAAG	2760
CTCTCACATC	GATAGGATCC	CATGAGGATG	GTCCCCTTCA	CCTGGGAGAA	AAGTGACCCA	2820
GTTTAGGAGC	TGGAGGGGGG	TCTTTGTCCC	CCACCCCCAA	ACTGCCCTGA	AATAAACCTG	2880
GAGTGAGCTG	CCCA					2894

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCTCGGAAT TCCGAGCTTG GATCCTCTAG AGCGGCCGCC GACTAGTGAG CTCGTCGACC
CGGGAATT

60
68

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AATTAATTCC CGGGTCGACG AGCTCACTAG TCGGCGGCCG CTCTAGAGGA TCCAAGCTCG
GAATTCCG

60
68

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGCGGATAAC AATTTACAC AGGA

24

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TGTAAAACGA CGGCCAGT

18

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAGAAGTCCC AGTCATCTGA TC

22

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AGAGGTCCTG GAAGCCATAC

20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGACTGTTG GGTTTTTCGT

20

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTCAAAGAGG GTGGCACAGA

20

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CTTTGTGTCC ACCAGGTGTG

20

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TCTGTGCCAC CCTCTTTGAC

20

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATCCTCCTCA CTGGCGTAGA

20

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AGAGTTCTCA TCTGGCGTTG

20

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAATCCTCTG GAAAACCCCT GAGC

24

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CCATTGCTCC TTCTTTCTCT GCCC

24

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met	Asp	Arg	Val	Thr	Arg	Tyr	Pro	Ile	Leu	Gly	Ile	Pro	Gln	Ala	His
1				5				10					15		
Arg	Gly	Thr	Gly	Leu	Val	Leu	Asp	Gly	Asp	Thr	Ser	Tyr	Thr	Tyr	His
			20					25					30		

)

```

Val Ala Glu Glu Arg Arg Asn Ala Leu Phe Pro Glu Val Phe Ser Pro
                    565                    570                    575
Thr Pro Asp Glu Asn Ser Asp Gln Asn Ser Arg Ser Ser Ser Gln Ala
                    580                    585                    590
Ser Gly Ile Thr Gly Ser Tyr Ser Val Ser Glu Ser Pro Phe Phe Ser
                    595                    600                    605
Pro Ile His Leu His Ser Asn Val Ala Trp Thr Val Glu Asp Pro Val
                    610                    615                    620
Asp Ser Ala Pro Pro Gly Gln Arg Lys Lys Glu Gln Trp Tyr Ala Gly
625                    630                    635                    640
Ile Asn Pro Ser Asp Gly Ile Asn Ser Glu Val Leu Glu Ala Ile Arg
                    645                    650                    655
Val Thr Arg His Lys Asn Ala Met Ala Glu Arg Trp Glu Ser Arg Ile
                    660                    665                    670
Tyr Ala Ser Glu Glu Asp Asp
                    675

```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```

Met Ser Pro Arg His Leu Ser Glu Ser Ser Gly Lys Pro Leu Ser Thr
 1          5          10          15
Lys Gln Glu Ala Ser Lys Pro Pro Arg Gly Cys Pro Gln Ala Asn Arg
          20          25          30
Gly Val Val Arg
          35

```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Arg Leu Gln Lys Ser Gln Ser Ser Asp Leu Leu Glu Arg Glu Arg Glu
 1          5          10          15
Ser Val Leu Arg Arg Glu Gln Glu Val Ala Glu Glu Arg Arg Asn
          20          25          30

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Met His Thr Glu His
1 5 10 15
His His His His His
20